Table 8. *MKKS/BBS6* Pathologic Allelic Variants

Gene	Mutation	Exon	Reference
BBS6	p.A242S heterozygote	3	Katsanis et al 2001
BBS6	p.Q147X heterozygote	3	Katsanis et al 2001
BBS6	p.Q147X heterozygote	3	Katsanis et al 2001
BBS6	p.Y37C homozygous	3	Katsanis et al 2001
BBS6	p.C499S heterozygote	6	Katsanis et al 2001
MKKS	p.H84Y homozygote	3	Stone et al 2000
MKKS	p.A242S homozygote	3	Stone et al 2000
MKKS	p.Y37C heterozygote	3	Stone et al 2000
MKKS	p.W405fsX413 heterozygote	5	Stone et al 2000
BBS6	p.Y37C homozygote	3	Katsanis et al 2000, Katsanis et al 2001
BBS6	p.D143fsX157 heterozygote	3	Katsanis et al 2000
BBS6	p.L227P heterozygote	3	Katsanis et al 2000
BBS6	p.F94fsX103 homozygote	3	Katsanis et al 2000, Slavotinek et al 2000
BBS6	p.D143fsX157 homozygote	3	Katsanis et al 2000, Slavotinek et al 2000
BBS6	p.F94fsX103 heterozygote	3	Katsanis et al 2000
BBS6	p.D143fsX157 heterozygote	3	Katsanis et al 2000
BBS6	p.T57A heterozygote	3	Katsanis et al 2000
BBS6	p.G52D heterozygote	3	Slavotinek et al 2000
BBS6	p.Y264X heterozygote	3	Slavotinek et al 2000
BBS6	p.A242S heterozygote	3	Beales et al 2001
BBS6	p.A242S heterozygote	3	Slavotinek et al 2000
BBS6	p.Q147X homozygote	3	Beales et al 2001
BBS6	p.D285A homozygote	3	Beales et al 2001
BBS6	p.R518H homozygote	6	Beales et al 2001
BBS6	p.I32M homozygote	3	Beales et al 2001
BBS6	p.S235P homozygote	3	Beales et al 2001
BBS6	p.C499S homozygote	6	Beales et al 2001

Gene	Mutation	Exon	Reference
BBS6	p.S511A homozygote	6	Beales et al 2001
BBS6	c.431-441del homozygote	3	Slavotinek et al 2002
BBS6	c.876-877 insCCTG heterozygote	3	Slavotinek et al 2002
BBS6	p.G345E homozygote	4	Slavotinek et al 2002
BBS6	p.R155L	3	Slavotinek et al 2002
BBS6	p.I339V	4	Slavotinek et al 2002

.0001 BBS6, H84Y. A homozygous histidine to tyrosine missense mutation was found together with A242S in all affected Amish individuals with McKusick-Kaufman syndrome [Stone et al 2000]. It has been predicted that this substitution may disrupt protein function by interfering with ATP hydrolysis in the equatorial domain of the protein.

.0002 BBS6, A242S. A homozygous alanine to serine missense mutation was found together with H84Y in all affected Amish individuals with Mckusick-Kaufman syndrome [Stone et al 2000]. However, unlike H84Y, this mutation has not been predicted to disrupt protein function. It has also been found in one unaffected control from Newfoundland [Beales et al 2001], in heterozygous form in an individual with BBS who had hypothyroidism [Slavotinek et al 2002], and in affected and unaffected siblings in a Newfoundland family [Katsanis et al 2001]. It has been proposed that either this allele is actually a rare polymorphism, or else that BBS arises through multiallelic inheritance [Katsanis et al 2001].

.0003 BBS6, Y37C. A tyrosine to cysteine missense mutation was found in an infant with MKKS in compound heterozygous form along with a two base pair deletion in exon 5 (W405fsX413) [Stone et al 2000]. Y37C was also identified in homozygous form in an individual with BBS who carried an additional mutation in the BBS2 gene (N70S) [Katsanis et al 2001].

.0004 BBS6, W405fsX413. This two base pair deletion in exon 5 of the BBS6 gene was found in compound heterozygous form with Y37C in an infant with MKKS [Stone et al 2000].

.0005 BBS6, D143fsX157. This mutation is a complex deletion that predicts the introduction of a premature termination codon at residue 157 of the BBS6 gene and was identified in homozygous form in all affected individuals from two Newfoundland BBS families [Katsanis et al 2000]. In addition, it was also found in compound heterozygous form in an affected individual together with D143fsX157, and with L227P in an affected individual from Newfoundland [Katsanis et al 2000].

.0006 BBS6, L227P. This missense mutation was found in compound heterozygous form in an affected individual from Newfoundland together with D143fsX157 [Katsanis et al 2000].

.0007 BBS6, F94fsX103. This mutation has been identified in the homozygous form in all affected individuals from three BBS families from Newfoundland [Katsanis et al 2000, Slavotinek et al 2000]. In addition, it was also found in compound heterozygous form in an affected individual together with D143fsX157 [Katsanis et al 2000].

.0008 BBS6, T57A. This missense mutation was identified in heterozygous form in an individual with BBS and was not found in 192 control chromosomes [Katsanis et al 2000].

.0009 BBS6, G52D. A Hispanic BBS proband was found to be a compound heterozygote for a glycine to aspartic acid missense mutation (G52D), and a nonsense mutation (Y264X) in BBS6 [Slavotinek et al 2000].

.0010 BBS6, Y264X. A Hispanic BBS proband was found to be a compound heterozygote for a nonsense mutation (Y264X), and a missense mutation (G52D) in BBS6 [Slavotinek et al 2000].

.0011 BBS6, Q147X. This nonsense mutation was identified in heterozygous form in an individual with BBS who also carried two nonsense mutations in the BBS2 gene (Y24X & Q59X) [Beales et al 2001, Katsanis et al 2001].

.0012 BBS6, D285A. This missense mutation was identified in homozygous form in affected individuals from a BBS pedigree [Beales et al 2001].

.0013 BBS6, R518H. This missense mutation was identified in homozygous form in affected individuals from a BBS pedigree [Beales et al 2001].

.0014 BBS6, I32M. This missense mutation was identified in homozygous form in affected individuals from a BBS pedigree [Beales et al 2001]. It was suggested that this would result in the introduction of an alternative methionine start codon.

.0015 BBS6, S235P. This missense mutation was identified in homozygous form in affected individuals from a BBS pedigree [Beales et al 2001]. It was suggested that this change would result in a structural change to the BBS6 protein.

.0016 BBS6, C499S. This missense mutation was identified in homozygous form in an individual with BBS along with two other nonsense mutations in the BBS6 gene (L168fsX170 and R216X) [Katsanis et al 2001].

.0017 BBS6, S511A. This missense mutation was identified in homozygous form in affected individuals from a BBS pedigree [Beales et al 2001].

.0018 BBS6, c.431-441del. A homozygous deletion of 10 base pairs in exon 3 of the BBS6 gene that predicts a frameshift resulting in a premature stop codon at residue 152 was identified in an individual with BBS [Slavotinek et al 2002].

.0019 BBS6, c.876-877insCCTG. A heterozygous insertion of 4 base pairs in exon 3 of BBS6 was identified that predicts a frameshift resulting in a premature stop codon at residue 327 in an individual with atypical BBS [Slavotinek et al 2002].

.0020 BBS6, p.G345E. This homozygous missense mutation was identified in an individual with BBS [Slavotinek et al 2002].

.0021 BBS6, p.R155L. This missense mutation was identified in heterozygous form in an individual with BBS [Slavotinek et al 2002].

.0022 BBS6, p.I339V. This missense mutation was identified in heterozygous form in an individual with BBS [Slavotinek et al 2002].